SEQUENCE LISTING

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(ii) TITLE OF INVENTION: NOVEL THERAPEUTIC MOLECULES

(iii) NUMBER OF SEQUENCES: 26

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(v) COMPUTER READABLE FORM:
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(B) COMPUTER: IBM PC compatible
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 333 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
ATG GCC AAG CAA CCT TCT GAT GTA AGT TCT GAG TGT GAC AGA GAA GGT        48
Met Ala Lys Gln Pro Ser Asp Val Ser Ser Glu Cys Asp Arg Glu Gly
 1               5                  10                  15

GGA CAA TTG CAG CCT GCT GAG AGG CCT CCC CAG CTC AGG CCT GGG GCC        96
Gly Gln Leu Gln Pro Ala Glu Arg Pro Pro Gln Leu Arg Pro Gly Ala
            20                  25                  30

CCT ACC TCC CTA CAG ACA GAA CCG CAA GCT TCC ATA CGA CAG TCT CAG       144
Pro Thr Ser Leu Gln Thr Glu Pro Gln Ala Ser Ile Arg Gln Ser Gln
        35                  40                  45

GAG GAA CCT GAA GAT CTG CGC CCG GAG ATA CGG ATT GCA CAG GAG CTG       192
Glu Glu Pro Glu Asp Leu Arg Pro Glu Ile Arg Ile Ala Gln Glu Leu
    50                  55                  60

CGG CGG ATC GGA GAC GAG TTC AAC GAA ACT TAC ACA AGG AGG GTG TTT       240
Arg Arg Ile Gly Asp Glu Phe Asn Glu Thr Tyr Thr Arg Arg Val Phe
65                  70                  75                  80

GCA AAT GAT TAC CGC GAG GCT GAA GAC CAC CCT CAA ATG GTT ATC TTA       288
Ala Asn Asp Tyr Arg Glu Ala Glu Asp His Pro Gln Met Val Ile Leu
                85                  90                  95

CAA CTG TTA CGC TTT ATC TTC CGT CTG GTA TGG AGA AGG CAT TG            333
Gln Leu Leu Arg Phe Ile Phe Arg Leu Val Trp Arg Arg His
            100                 105                 110
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 110 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Met Ala Lys Gln Pro Ser Asp Val Ser Ser Glu Cys Asp Arg Glu Gly
 1               5                  10                  15

Gly Gln Leu Gln Pro Ala Glu Arg Pro Pro Gln Leu Arg Pro Gly Ala
            20                  25                  30

Pro Thr Ser Leu Gln Thr Glu Pro Gln Ala Ser Ile Arg Gln Ser Gln
        35                  40                  45

Glu Glu Pro Glu Asp Leu Arg Pro Glu Ile Arg Ile Ala Gln Glu Leu
    50                  55                  60

Arg Arg Ile Gly Asp Glu Phe Asn Glu Thr Tyr Thr Arg Arg Val Phe
65                  70                  75                  80

Ala Asn Asp Tyr Arg Glu Ala Glu Asp His Pro Gln Met Val Ile Leu
                85                  90                  95

Gln Leu Leu Arg Phe Ile Phe Arg Leu Val Trp Arg Arg His
            100                 105                 110
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 423 nucleotides
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
ATG GCC AAG CAA CCT TCT GAT GTA AGT TCT GAG TGT GAC AGA GAA GGT      48
Met Ala Lys Gln Pro Ser Asp Val Ser Ser Glu Cys Asp Arg Glu Gly
 1               5                  10                  15

GGA CAA TTG CAG CCT GCT GAG AGG CCT CCC CAG CTC AGG CCT GGG GCC      96
Gly Gln Leu Gln Pro Ala Glu Arg Pro Pro Gln Leu Arg Pro Gly Ala
            20                  25                  30

CCT ACC TCC CTA CAG ACA GAA CCG CAA GAC AGG AGC CCG GCA CCC ATG     144
Pro Thr Ser Leu Gln Thr Glu Pro Gln Asp Arg Ser Pro Ala Pro Met
        35                  40                  45

AGT TGT GAC AAG TCA ACA CAA ACC CCA AGT CCT CCT TGC CAG GCC TTC     192
Ser Cys Asp Lys Ser Thr Gln Thr Pro Ser Pro Pro Cys Gln Ala Phe
    50                  55                  60

AAC CAC TAT CTC AGT GCA ATG GCT TCC ATA CGA CAG TCT CAG GAG GAA     240
Asn His Tyr Leu Ser Ala Met Ala Ser Ile Arg Gln Ser Gln Glu Glu
65                  70                  75                  80

CCT GAA GAT CTG CGC CCG GAG ATA CGG ATT GCA CAG GAG CTG CGG CGG     288
Pro Glu Asp Leu Arg Pro Glu Ile Arg Ile Ala Gln Glu Leu Arg Arg
                85                  90                  95

ATC GGA GAC GAG TTC AAC GAA ACT TAC ACA AGG AGG GTG TTT GCA AAT     336
Ile Gly Asp Glu Phe Asn Glu Thr Tyr Thr Arg Arg Val Phe Ala Asn
            100                 105                 110

GAT TAC CGC GAG GCT GAA GAC CAC CCT CAA ATG GTT ATC TTA CAA CTG     384
Asp Tyr Arg Glu Ala Glu Asp His Pro Gln Met Val Ile Leu Gln Leu
        115                 120                 125
```

TTA CGC TTT ATC TTC CGT CTG GTA TGG AGA AGG CAT TG 423
Leu Arg Phe Ile Phe Arg Leu Val Trp Arg Arg His
130 135 140

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 140 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Lys Gln Pro Ser Asp Val Ser Ser Glu Cys Asp Arg Glu Gly
1 5 10 15

Gly Gln Leu Gln Pro Ala Glu Arg Pro Pro Gln Leu Arg Pro Gly Ala
20 25 30

Pro Thr Ser Leu Gln Thr Glu Pro Gln Asp Arg Ser Pro Ala Pro Met
35 40 45

Ser Cys Asp Lys Ser Thr Gln Thr Pro Ser Pro Pro Cys Gln Ala Phe
50 55 60

Asn His Tyr Leu Ser Ala Met Ala Ser Ile Arg Gln Ser Gln Glu Glu
65 70 75 80

Pro Glu Asp Leu Arg Pro Glu Ile Arg Ile Ala Gln Glu Leu Arg Arg
85 90 95

Ile Gly Asp Glu Phe Asn Glu Thr Tyr Thr Arg Arg Val Phe Ala Asn
100 105 110

Asp Tyr Arg Glu Ala Glu Asp His Pro Gln Met Val Ile Leu Gln Leu
115 120 125

Leu Arg Phe Ile Phe Arg Leu Val Trp Arg Arg His
130 135 140

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 591 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
ATG GCC AAG CAA CCT TCT GAT GTA AGT TCT GAG TGT GAC AGA GAA GGT        48
Met Ala Lys Gln Pro Ser Asp Val Ser Ser Glu Cys Asp Arg Glu Gly
 1               5                  10                  15

GGA CAA TTG CAG CCT GCT GAG AGG CCT CCC CAG CTC AGG CCT GGG GCC        96
Gly Gln Leu Gln Pro Ala Glu Arg Pro Pro Gln Leu Arg Pro Gly Ala
            20                  25                  30

CCT ACC TCC CTA CAG ACA GAA CCG CAA GGT AAT CCC GAC GGC GAA GGG       144
Pro Thr Ser Leu Gln Thr Glu Pro Gln Gly Asn Pro Asp Gly Glu Gly
        35                  40                  45

GAC CGC TGC CCC CAC GGC AGC CCT CAG GGC CCG CTG GCC CCA CCG GCC       192

Asp Arg Cys Pro His Gly Ser Pro Gln Gly Pro Leu Ala Pro Pro Ala
    50                  55                  60

AGC CCT GGC CCT TTT GCT ACC AGA TCC CCA CTT TTC ATC TTT GTG AGA       240
Ser Pro Gly Pro Phe Ala Thr Arg Ser Pro Leu Phe Ile Phe Val Arg
65                  70                  75                  80

AGA TCT TCT CTG CTG TCC CGG TCC TCC AGT GGG TAT TTC TCT TTT GAC       288
Arg Ser Ser Leu Leu Ser Arg Ser Ser Ser Gly Tyr Phe Ser Phe Asp
                85                  90                  95

ACA GAC AGG AGC CCG GCA CCC ATG AGT TGT GAC AAG TCA ACA CAA ACC       336
Thr Asp Arg Ser Pro Ala Pro Met Ser Cys Asp Lys Ser Thr Gln Thr
```

```
                100                 105                 110

CCA AGT CCT CCT TGC CAG GCC TTC AAC CAC TAT CTC AGT GCA ATG GCT      384
Pro Ser Pro Pro Cys Gln Ala Phe Asn His Tyr Leu Ser Ala Met Ala
        115                 120                 125

TCC ATA CGA CAG TCT CAG GAG GAA CCT GAA GAT CTG CGC CCG GAG ATA      432
Ser Ile Arg Gln Ser Gln Glu Glu Pro Glu Asp Leu Arg Pro Glu Ile
    130                 135                 140

CGG ATT GCA CAG GAG CTG CGG CGG ATC GGA GAC GAG TTC AAC GAA ACT      480
Arg Ile Ala Gln Glu Leu Arg Arg Ile Gly Asp Glu Phe Asn Glu Thr
145                 150                 155                 160

TAC ACA AGG AGG GTG TTT GCA AAT GAT TAC CGC GAG GCT GAA GAC CAC      528
Tyr Thr Arg Arg Val Phe Ala Asn Asp Tyr Arg Glu Ala Glu Asp His
                165                 170                 175

CCT CAA ATG GTT ATC TTA CAA CTG TTA CGC TTT ATC TTC CGT CTG GTA      576
Pro Gln Met Val Ile Leu Gln Leu Leu Arg Phe Ile Phe Arg Leu Val
            180                 185                 190

TGG AGA AGG CAT TG                                               591
Trp Arg Arg His
        195
```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 196 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Met Ala Lys Gln Pro Ser Asp Val Ser Ser Glu Cys Asp Arg Glu Gly
 1               5                  10                  15

Gly Gln Leu Gln Pro Ala Glu Arg Pro Pro Gln Leu Arg Pro Gly Ala
            20                  25                  30

Pro Thr Ser Leu Gln Thr Glu Pro Gln Gly Asn Pro Asp Gly Glu Gly
        35                  40                  45

Asp Arg Cys Pro His Gly Ser Pro Gln Gly Pro Leu Ala Pro Pro Ala
    50                  55                  60

Ser Pro Gly Pro Phe Ala Thr Arg Ser Pro Leu Phe Ile Phe Val Arg
65                  70                  75                  80

Arg Ser Ser Leu Leu Ser Arg Ser Ser Ser Gly Tyr Phe Ser Phe Asp
                85                  90                  95

Thr Asp Arg Ser Pro Ala Pro Met Ser Cys Asp Lys Ser Thr Gln Thr
            100                 105                 110

Pro Ser Pro Pro Cys Gln Ala Phe Asn His Tyr Leu Ser Ala Met Ala
        115                 120                 125

Ser Ile Arg Gln Ser Gln Glu Glu Pro Glu Asp Leu Arg Pro Glu Ile
    130                 135                 140

Arg Ile Ala Gln Glu Leu Arg Arg Ile Gly Asp Glu Phe Asn Glu Thr
145                 150                 155                 160

Tyr Thr Arg Arg Val Phe Ala Asn Asp Tyr Arg Glu Ala Glu Asp His
                165                 170                 175

Pro Gln Met Val Ile Leu Gln Leu Leu Arg Phe Ile Phe Arg Leu Val
            180                 185                 190

Trp Arg Arg His
        195
```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 417 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
ATG GCA AAG CAA CCT TCT GAT GTA AGT TCT GAG TGT GAC CGA GAA GGT        48
Met Ala Lys Gln Pro Ser Asp Val Ser Ser Glu Cys Asp Arg Glu Gly
 1               5                  10                  15

AGA CAA TTG CAG CCT GCG GAG AGG CCT CCC CAG CTC AGA CCT GGG GCC        96
Arg Gln Leu Gln Pro Ala Glu Arg Pro Pro Gln Leu Arg Pro Gly Ala
            20                  25                  30

CCT ACC TCC CTA CAG ACA GAG CCA CAA GAC AGG AGC CCA GCA CCC ATG       144
Pro Thr Ser Leu Gln Thr Glu Pro Gln Asp Arg Ser Pro Ala Pro Met
        35                  40                  45

AGT TGT GAC AAA TCA ACA CAA ACC CCA AGT CCT CCT TGC CAG GCC TTC       192
Ser Cys Asp Lys Ser Thr Gln Thr Pro Ser Pro Pro Cys Gln Ala Phe
    50                  55                  60

AAC CAC TAT CTC AGT GCA ATG GCT TCC ATG AGG CAG GCT GAA CCT GCA       240
Asn His Tyr Leu Ser Ala Met Ala Ser Met Arg Gln Ala Glu Pro Ala
65                  70                  75                  80

GAT ATG CGC CCA GAG ATA TGG ATC GCC CAA GAG TTG CGG CGT ATC GGA       288
Asp Met Arg Pro Glu Ile Trp Ile Ala Gln Glu Leu Arg Arg Ile Gly
                85                  90                  95

GAC GAG TTT AAC GCT TAC TAT GCA AGG AGG GTA TTT TTG AAT AAT TAC       336
Asp Glu Phe Asn Ala Tyr Tyr Ala Arg Arg Val Phe Leu Asn Asn Tyr
            100                 105                 110
```

```
CAA GCA GCC GAA GAC CAC CCA CGA ATG GTT ATC TTA CGA CTG TTA CGT      384
Gln Ala Ala Glu Asp His Pro Arg Met Val Ile Leu Arg Leu Leu Arg
        115                 120                 125

TAC ATT GTC CGC CTG GTG TGG AGA ATG CAT TG                          417
Tyr Ile Val Arg Leu Val Trp Arg Met His
    130                 135
```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 138 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
Met Ala Lys Gln Pro Ser Asp Val Ser Ser Glu Cys Asp Arg Glu Gly
  1               5                  10                  15

Arg Gln Leu Gln Pro Ala Glu Arg Pro Pro Gln Leu Arg Pro Gly Ala
             20                  25                  30

Pro Thr Ser Leu Gln Thr Glu Pro Gln Asp Arg Ser Pro Ala Pro Met
         35                  40                  45

Ser Cys Asp Lys Ser Thr Gln Thr Pro Ser Pro Pro Cys Gln Ala Phe
     50                  55                  60

Asn His Tyr Leu Ser Ala Met Ala Ser Met Arg Gln Ala Glu Pro Ala
 65                  70                  75                  80

Asp Met Arg Pro Glu Ile Trp Ile Ala Gln Glu Leu Arg Arg Ile Gly
                 85                  90                  95

Asp Glu Phe Asn Ala Tyr Tyr Ala Arg Arg Val Phe Leu Asn Asn Tyr
            100                 105                 110

Gln Ala Ala Glu Asp His Pro Arg Met Val Ile Leu Arg Leu Leu Arg
        115                 120                 125
```

```
Tyr Ile Val Arg Leu Val Trp Arg Met His
    130                 135
```

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 597 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..597

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
ATG GCA AAG CAA CCT TCT GAT GTA AGT TCT GAG TGT GAC CGA GAA GGT        48
Met Ala Lys Gln Pro Ser Asp Val Ser Ser Glu Cys Asp Arg Glu Gly
  1               5                  10                  15

AGA CAA TTG CAG CCT GCG GAG AGG CCT CCC CAG CTC AGA CCT GGG GCC        96
Arg Gln Leu Gln Pro Ala Glu Arg Pro Pro Gln Leu Arg Pro Gly Ala
             20                  25                  30

CCT ACC TCC CTA CAG ACA GAG CCA CAA GGT AAT CCT GAA GGC AAT CAC       144
Pro Thr Ser Leu Gln Thr Glu Pro Gln Gly Asn Pro Glu Gly Asn His
         35                  40                  45

GGA GGT GAA GGG GAC AGC TGC CCC CAC GGC AGC CCT CAG GGC CCG CTG       192
Gly Gly Glu Gly Asp Ser Cys Pro His Gly Ser Pro Gln Gly Pro Leu
     50                  55                  60

GCC CCA CCT GCC AGC CCT GGC CCT TTT GCT ACC AGA TCC CCG CTT TTC       240
Ala Pro Pro Ala Ser Pro Gly Pro Phe Ala Thr Arg Ser Pro Leu Phe
 65                  70                  75                  80

ATC TTT ATG AGA AGA TCC TCC CTG CTG TCT CGA TCC TCC AGT GGG TAT       288
Ile Phe Met Arg Arg Ser Ser Leu Leu Ser Arg Ser Ser Ser Gly Tyr
                 85                  90                  95
```

```
TTC TCT TTT GAC ACA GAC AGG AGC CCA GCA CCC ATG AGT TGT GAC AAA      336
Phe Ser Phe Asp Thr Asp Arg Ser Pro Ala Pro Met Ser Cys Asp Lys
            100                 105                 110

TCA ACA CAA ACC CCA AGT CCT CCT TGC CAG GCC TTC AAC CAC TAT CTC      384
Ser Thr Gln Thr Pro Ser Pro Pro Cys Gln Ala Phe Asn His Tyr Leu
        115                 120                 125

AGT GCA ATG GCT TCC ATG AGG CAG GCT GAA CCT GCA GAT ATG CGC CCA      432
Ser Ala Met Ala Ser Met Arg Gln Ala Glu Pro Ala Asp Met Arg Pro
    130                 135                 140

GAG ATA TGG ATC GCC CAA GAG TTG CGG CGT ATC GGA GAC GAG TTT AAC      480
Glu Ile Trp Ile Ala Gln Glu Leu Arg Arg Ile Gly Asp Glu Phe Asn
145                 150                 155                 160

GCT TAC TAT GCA AGG AGG GTA TTT TTG AAT AAT TAC CAA GCA GCC GAA      528
Ala Tyr Tyr Ala Arg Arg Val Phe Leu Asn Asn Tyr Gln Ala Ala Glu
                165                 170                 175

GAC CAC CCA CGA ATG GTT ATC TTA CGA CTG TTA CGT TAC ATT GTC CGC      576
Asp His Pro Arg Met Val Ile Leu Arg Leu Leu Arg Tyr Ile Val Arg
            180                 185                 190

CTG GTG TGG AGA ATG CAT TG                                          597
Leu Val Trp Arg Met His
        195
```

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 198 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```
Met Ala Lys Gln Pro Ser Asp Val Ser Ser Glu Cys Asp Arg Glu Gly
  1               5                  10                  15
```

```
Arg Gln Leu Gln Pro Ala Glu Arg Pro Pro Gln Leu Arg Pro Gly Ala
          20                  25                  30

Pro Thr Ser Leu Gln Thr Glu Pro Gln Gly Asn Pro Glu Gly Asn His
      35                  40                  45

Gly Gly Glu Gly Asp Ser Cys Pro His Gly Ser Pro Gln Gly Pro Leu
  50                  55                  60

Ala Pro Pro Ala Ser Pro Gly Pro Phe Ala Thr Arg Ser Pro Leu Phe
65                  70                  75                  80

Ile Phe Met Arg Arg Ser Ser Leu Leu Ser Arg Ser Ser Ser Gly Tyr
                85                  90                  95

Phe Ser Phe Asp Thr Asp Arg Ser Pro Ala Pro Met Ser Cys Asp Lys
            100                 105                 110

Ser Thr Gln Thr Pro Ser Pro Pro Cys Gln Ala Phe Asn His Tyr Leu
        115                 120                 125

Ser Ala Met Ala Ser Met Arg Gln Ala Glu Pro Ala Asp Met Arg Pro
    130                 135                 140

Glu Ile Trp Ile Ala Gln Glu Leu Arg Arg Ile Gly Asp Glu Phe Asn
145                 150                 155                 160

Ala Tyr Tyr Ala Arg Arg Val Phe Leu Asn Asn Tyr Gln Ala Ala Glu
                165                 170                 175

Asp His Pro Arg Met Val Ile Leu Arg Leu Leu Arg Tyr Ile Val Arg
            180                 185                 190

Leu Val Trp Arg Met His
        195
```

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Glu Tyr Met Pro Met Glu
1 5

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Leu Arg Arg Ile Gly Asp Glu
1 5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGGGAGAACA GGGTACATCG ATGCGGG 27

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GTGAACTGGG AGCGGATTGT GG 22

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CACCTGCACA CCGCGATCCA GGATAACG 28

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGGATCCACC ATGGCCAAGC AACC 24

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GTTCTAGATC AGCACATCTC TCTGGGATAG AACCAC 36

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GCAAGCTTCCT GTGCAATCCG TATCTCC 27

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGAAGCTTGC AACGAAACTT ACACAAGGTG 30

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCAAGCTTCC GGGCGCAGAT CTTC 24

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CAAAGCTTCC TGTGCAATCC GTATCTCC 28

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGAAGCTTTG AACGAAACTT ACACAAGGTG 30

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CAAAGCTTCC GGGCGCAGAT CTTC 23

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TAAGTTCTGA GTGTGACAGA GAAGGTGG 28

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CAGTTGTAAG ATAACCATTT GAGGGTGG 28